

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/536,772
Source: PKT
Date Processed by STIC: 6/13/05

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ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/S36,772

CRF Edit Date: 6/13/05
Edited by: Zel

Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Deleted: invalid beginning/end-of-file text ; page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other:

Raw Sequence Listing before editing,
for reference only



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/536,772

DATE: 06/13/2005
TIME: 15:05:39

Input Set : A:\pto.kd.txt
Output Set: N:\CRF4\06132005\J536772.raw

4 <110> APPLICANT: SHANGHAI CANCER INSTITUTE
6 <120> TITLE OF INVENTION: A HUMAN TUMOR-ASSOCIATED GENE CT120 ON CHROMOSOME 17P 13.3
REGION AND

7 PROTEIN
8 ENCODED BY IT
10 <130> FILE REFERENCE: 024832pc
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/536,772
C--> 12 <141> CURRENT FILING DATE: 2005-05-26
12 <150> PRIOR APPLICATION NUMBER: CN 02150730.9
13 <151> PRIOR FILING DATE: 2002-11-27
15 <160> NUMBER OF SEQ ID NOS: 13
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2145
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (91)..(861)
27 <223> OTHER INFORMATION:
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30 cggagggttg aaatcgcgcg gcccggccgg ggcgcgcga gccgaaccca gccacgcggc 60
31 gccagcgagg cggccggacc cgcagccccc atg ctg ctg acg ctg gcc ggg ggc 114
32 Met Leu Leu Thr Leu Ala Gly Gly
33 1 5
34 gcg ctc ttc ttc ccg ggg ctc ttc gcg ctc tgc acc tgg gcg ctg cgc 162
35 Ala Leu Phe Phe Pro Gly Leu Phe Ala Leu Cys Thr Trp Ala Leu Arg
36 10 15 20
37 cac tcc cag ccc gga tgg agc cgc acc gac tgc gtg atg atc agc acc 210
38 His Ser Gln Pro Gly Trp Ser Arg Thr Asp Cys Val Met Ile Ser Thr
39 25 30 35 40
40 agg ctg gtt tcc tcg gtg cac gcc gtg ctg gcc acc ggc tcg ggg atc 258
41 Arg Leu Val Ser Val His Ala Val Leu Ala Thr Gly Ser Gly Ile
42 45 50 55
43 gtc atc att cgc tcc tgc gac gac gtg atc acc ggc agg cac tgg ctt 306
44 Val Ile Ile Arg Ser Cys Asp Asp Val Ile Thr Gly Arg His Trp Leu
45 60 65 70
46 gcc cgg gaa tat gtg tgg ttt ctg att cca tac atg atc tat gac tcg 354
47 Ala Arg Glu Tyr Val Trp Phe Leu Ile Pro Tyr Met Ile Tyr Asp Ser
48 75 80 85
49 tac gcc atg tac ctc tgt gaa tgg tgc cga acc aga gac cag aac cgt 402
50 Tyr Ala Met Tyr Leu Cys Glu Trp Cys Arg Thr Arg Asp Gln Asn Arg
51 90 95 100
52 gcg ccc tcc ctc act ctt cga aac ttc cta agt cga aac aac cgc ctc atg 450

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53	Ala	Pro	Ser	Leu	Thr	Leu	Arg	Asn	Phe	Leu	Ser	Arg	Asn	Arg	Leu	Met			
54	105				110					115						120			
55	atc	aca	cat	cat	gct	att	ctc	ctt	gtc	ctt	gtg	cca	gtc	gca	cag		498		
56	Ile	Thr	His	His	Ala	Val	Ile	Leu	Leu	Val	Leu	Val	Pro	Val	Ala	Gln			
57					125					130						135			
58	agg	ctc	cgg	gga	gac	ctt	ggg	gac	ttc	ttt	gtc	ggc	tgc	atc	ttc	acg		546	
59	Arg	Leu	Arg	Gly	Asp	Leu	Gly	Asp	Phe	Phe	Val	Gly	Cys	Ile	Phe	Thr			
60					140					145						150			
61	gca	gaa	ctg	agc	act	ccg	ttt	gtg	tcg	ctg	ggc	agg	gtt	ctg	att	cag		594	
62	Ala	Glu	Leu	Ser	Thr	Pro	Phe	Val	Ser	Leu	Gly	Arg	Val	Leu	Ile	Gln			
63					155					160						165			
64	cta	aag	cag	cag	cac	acc	ctt	ctg	tac	aag	gtg	aat	gga	atc	ctc	acg		642	
65	Leu	Lys	Gln	Gln	His	Thr	Leu	Leu	Tyr	Lys	Val	Asn	Gly	Ile	Leu	Thr			
66					170					175						180			
67	ctg	gcc	acc	ttc	ctt	tcc	tgc	cg	atc	ctt	ctc	ccc	ttc	atg	tac		690		
68	Leu	Ala	Thr	Phe	Leu	Ser	Cys	Arg	Ile	Leu	Leu	Phe	Pro	Phe	Met	Tyr			
69					185					190						195			
70	tgg	tcc	tat	ggc	cgc	cag	cag	gga	cta	agc	ctg	ctc	caa	gta	ccc	ttc		738	
71	Trp	Ser	Tyr	Gly	Arg	Gln	Gln	Gly	Leu	Ser	Leu	Leu	Gln	Val	Pro	Phe			
72					205					210						215			
73	agc	atc	cca	ttc	tac	tgc	aac	gtg	gcc	aat	gcc	ttc	ctc	gta	gct	cct		786	
74	Ser	Ile	Pro	Phe	Tyr	Cys	Asn	Val	Ala	Asn	Ala	Phe	Leu	Val	Ala	Pro			
75					220					225						230			
76	cag	atc	tac	tgg	ttc	tgt	ctg	tgc	agg	aag	gca	gtc	cg	ctc	ttt		834		
77	Gln	Ile	Tyr	Trp	Phe	Cys	Leu	Leu	Cys	Arg	Lys	Ala	Val	Arg	Leu	Phe			
78					235					240						245			
79	gac	act	ccc	caa	gcc	aaa	aag	gat	ggc	taaatgctcc	ttggagtcag							881	
80	Asp	Thr	Pro	Gln	Ala	Lys	Lys	Asp	Gly										
81					250					255									
82	gcgcagcctc	acaccagctg	cctcctccac	tcagcattcc													941		
83	ggtagcctca	gactttgggt	attgataagc	cgatggattt													1001		
84	catattac	cctttttctta	acttgcctca	tttgc当地acg	cacttttgc当地												1061		
85	ttgggtcctg	tcagac	tc	acggac	agca	aagtgtttt	aat	gcaag	cc	caaggat	cct						1121		
86	tcttaagg	tc	ttatctcaag	agctctgg	ggtggaa	gca	ttgggtgg	tcgg	ttgg	tc	ttgg	ttgg	ttgg	ttgg	ttgg		1181		
87	agggtggtaa	gtgt	ctgcac	atctgcctgt	ccctgtatca	gcgg	gtatccac	ac	tttcc	tttcc	tttcc	tttcc	tttcc	tttcc	tttcc		1241		
88	ccactcagga	cag	tacc	ccgt	ggca	act	gggg	cc	ggca	ggca	ggca	ggca	ggca	ggca	ggca		1301		
89	gaagtaatgt	cgt	ttgt	gt	catt	ggcc	ct	gg	acaat	cat	tgt	gggt	tag	ttt	att	ga	1361		
90	tcgttacta	gata	acc	cat	ttgt	tttt	cct	cata	c	tat	ccat	gg	tc	ca	gg	ttt	1421		
91	aattctttag	tct	at	ta	gact	tcca	at	ca	tc	at	tc	tt	gg	tt	gg	ttt	1481		
92	aggcaggagg	cat	ggat	ggg	aa	cct	tgat	g	gt	at	tt	gg	tt	gg	tt	gg	1541		
93	ttgcaggctg	actt	gct	ta	ac	tt	gc	at	gt	tt	at	tc	tt	tc	at	tc	1601		
94	cagaggctgt	tct	ttt	tc	ac	ccc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1661		
95	aggcgagct	cata	aaa	acta	cagg	ga	cg	tg	aa	at	gt	tt	gg	tt	at	ct	1721		
96	ggt	ta	ac	cc	act	gt	cc	ttt	ca	t	gt	at	gt	gg	at	tc	1781		
97	aaccatgaaa	tgt	gt	cat	ct	ag	at	gc	ag	tc	gt	tt	gg	at	gg	tc	1841		
98	agagcttgtg	gt	cc	aa	ag	cc	catt	ct	tgt	gt	tt	gg	at	tc	gg	at	1901		
99	tgccggagt	ga	gg	ccgg	cag	ct	gg	ct	gt	gg	ct	gg	ac	cc	gg	cc	1961		
100	cccttctgca	agc	agg	attt	tct	gg	tc	ca	act	catt	tc	at	catt	cc	at	ca	act	agg	2021
101	atgaatttaa	gac	tgt	gct	ca	at	gt	gt	tc	ta	gg	tt	aa	aa	ag	tg	ttt	tttta	2081

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102 aagtgccttt caattgtctg tgaacgtcta aaggactgat ttgtctcaa aaaaaaaaaa 2141
103 aaaa 2145
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 257
107 <212> TYPE: PRT
108 <213> ORGANISM: Homo sapiens
110 <400> SEQUENCE: 2
111 Met Leu Leu Thr Leu Ala Gly Gly Ala Leu Phe Phe Pro Gly Leu Phe
112 1 5 10 15
113 Ala Leu Cys Thr Trp Ala Leu Arg His Ser Gln Pro Gly Trp Ser Arg
114 20 25 30
115 Thr Asp Cys Val Met Ile Ser Thr Arg Leu Val Ser Ser Val His Ala
116 35 40 45
117 Val Leu Ala Thr Gly Ser Gly Ile Val Ile Ile Arg Ser Cys Asp Asp
118 50 55 60
119 Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu
120 65 70 75 80
121 Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp
122 85 90 95
123 Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn
124 100 105 110
125 Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu
126 115 120 125
127 Leu Val Leu Val Pro Val Ala Gln Arg Leu Arg Gly Asp Leu Gly Asp
128 130 135 140
129 Phe Phe Val Gly Cys Ile Phe Thr Ala Glu Leu Ser Thr Pro Phe Val
130 145 150 155 160
131 Ser Leu Gly Arg Val Leu Ile Gln Leu Lys Gln Gln His Thr Leu Leu
132 165 170 175
133 Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg
134 180 185 190
135 Ile Leu Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly
136 195 200 205
137 Leu Ser Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val
138 210 215 220
139 Ala Asn Ala Phe Leu Val Ala Pro Gln Ile Tyr Trp Phe Cys Leu Leu
140 225 230 235 240
141 Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys Asp
142 245 250 255
143 Gly
146 <210> SEQ ID NO: 3
147 <211> LENGTH: 25
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial
151 <220> FEATURE:
152 <221> NAME/KEY: misc_feature
153 <222> LOCATION: (1)..(25)
154 <223> OTHER INFORMATION: primer
156 <400> SEQUENCE: 3

RAW SEQUENCE LISTING
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Input Set : A:\pto.kd.txt
Output Set: N:\CRF4\06132005\J536772.raw

157 gtgcgactgg cacaaggaca aagag	25
159 <210> SEQ ID NO: 4	
160 <211> LENGTH: 23	
161 <212> TYPE: DNA	
162 <213> ORGANISM: Artificial	
164 <220> FEATURE:	
165 <221> NAME/KEY: misc_feature	
166 <222> LOCATION: (1)..(23)	
167 <223> OTHER INFORMATION: primer	
169 <400> SEQUENCE: 4	
170 cgaatgatga cgatcccgaa gcc	23
172 <210> SEQ ID NO: 5	
173 <211> LENGTH: 22	
174 <212> TYPE: DNA	
175 <213> ORGANISM: Artificial	
177 <220> FEATURE:	
178 <221> NAME/KEY: misc_feature	
179 <222> LOCATION: (1)..(22)	
180 <223> OTHER INFORMATION: primer	
182 <400> SEQUENCE: 5	
183 ccgatgctgc tgacgctggc cg	22
185 <210> SEQ ID NO: 6	
186 <211> LENGTH: 25	
187 <212> TYPE: DNA	
188 <213> ORGANISM: Artificial	
190 <220> FEATURE:	
191 <221> NAME/KEY: misc_feature	
192 <222> LOCATION: (1)..(25)	
193 <223> OTHER INFORMATION: primer	
195 <400> SEQUENCE: 6	
196 tgttggcacc agaaaatcct gcttg	25
198 <210> SEQ ID NO: 7	
199 <211> LENGTH: 20	
200 <212> TYPE: DNA	
201 <213> ORGANISM: Artificial	
203 <220> FEATURE:	
204 <221> NAME/KEY: misc_feature	
205 <222> LOCATION: (1)..(20)	
206 <223> OTHER INFORMATION: primer	
208 <400> SEQUENCE: 7	
209 aagtactccg tgtggatcg	20
211 <210> SEQ ID NO: 8	
212 <211> LENGTH: 20	
213 <212> TYPE: DNA	
214 <213> ORGANISM: Artificial	
216 <220> FEATURE:	
217 <221> NAME/KEY: misc_feature	
218 <222> LOCATION: (1)..(20)	
219 <223> OTHER INFORMATION: primer	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/536,772

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Input Set : A:\pto.kd.txt
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221 <400> SEQUENCE: 8
222 tcaagttggg ggacaaaaag 20
224 <210> SEQ ID NO: 9
225 <211> LENGTH: 25
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial
229 <220> FEATURE:
230 <221> NAME/KEY: misc_feature
231 <222> LOCATION: (1)..(25)
232 <223> OTHER INFORMATION: primer
234 <400> SEQUENCE: 9
235 gtgcgactgg cacaaggaca aagag 25
237 <210> SEQ ID NO: 10
238 <211> LENGTH: 23
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial
242 <220> FEATURE:
243 <221> NAME/KEY: misc_feature
244 <222> LOCATION: (1)..(23)
245 <223> OTHER INFORMATION: primer
247 <400> SEQUENCE: 10
248 ggggatcgtc atcatcgct cct 23
250 <210> SEQ ID NO: 11
251 <211> LENGTH: 15
252 <212> TYPE: PRT
253 <213> ORGANISM: Artificial
255 <220> FEATURE:
256 <221> NAME/KEY: MISC_FEATURE
257 <222> LOCATION: (1)..(15)
258 <223> OTHER INFORMATION: oligopeptide corresponding to C-terminus of CT120 protein
260 <400> SEQUENCE: 11
262 Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys
263 1 5 10 15
265 <210> SEQ ID NO: 12
266 <211> LENGTH: 20
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial
270 <220> FEATURE:
271 <221> NAME/KEY: misc_feature
272 <222> LOCATION: (1)..(20)
273 <223> OTHER INFORMATION: primer
275 <400> SEQUENCE: 12
276 atgctgctga cgctggccgg 20
278 <210> SEQ ID NO: 13
279 <211> LENGTH: 20
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial
283 <220> FEATURE:
284 <221> NAME/KEY: misc_feature

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/536,772

DATE: 06/13/2005
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Input Set : A:\pto.kd.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/536,772**

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Input Set : **A:\pto.kd.txt**
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27